

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 04:07:44 ; Search time 4678 Seconds
(without alignments)
11220.268 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%		Query		DB		ID	Description
No.	Score	Match	Length	DB	ID				
1	1211	100.0	1211	6	AX394331	60 02/18599	AX394331	Sequence	
2	1211	100.0	309400	6	AX127153	EP 1108770	AX127153	Sequence	
3	1211	100.0	325651	1	AP005283	GenBank	AP005283	Corynebact	
4	603	49.8	603	6	AX123500		AX123500	Sequence	
5	603	49.8	603	6	BD165617		BD165617	Novel pol	
c 6	449	37.1	1185	6	AX123502		AX123502	Sequence	
c 7	449	37.1	1185	6	BD165619		BD165619	Novel pol	
8	243.6	20.1	87340	1	AP005224		AP005224	Corynebact	
9	197	16.3	951	6	AX123501		AX123501	Sequence	
10	197	16.3	951	6	BD165618		BD165618	Novel pol	
11	194.8	16.1	53793	1	BX248361		BX248361	Corynebact	
12	96.8	8.0	1775	1	AF023161		AF023161	Mycobacte	
13	82	6.8	210205	1	AY223810		AY223810	Rhodococc	
c 14	79.6	6.6	1443	6	AR227225		AR227225	Sequence	
15	79.6	6.6	302988	1	AE017176		AE017176	Porphyrom	
16	79	6.5	1800	1	MLTRTRXHP		X87899 M.leprae TR		
17	79	6.5	40571	1	MSGDNAB		L39923 Mycobacteri		
18	79	6.5	269203	1	MLEPRTN10		AL583926 Mycobacte		
19	78	6.4	3457	6	AX764249		AX764249	Sequence	
20	78	6.4	3457	6	AX773631		AX773631	Sequence	
21	77.6	6.4	300956	1	AE016963		AE016963	Coxiella	
22	75	6.2	1529	1	MTTRTRXGN		X95798 M.tuberculo		
23	75	6.2	9882	1	AE007194		AE007194	Mycobacte	
24	75	6.2	10940	1	AE009169		AE009169	Agrobacte	
25	75	6.2	12357	1	AE008135		AE008135	Agrobacte	
c 26	75	6.2	35336	1	MSGY367		AD000008 Mycobacte		
27	75	6.2	244800	1	BX842584		BX842584	Mycobacte	
28	73.4	6.1	278492	1	BX248347		BX248347	Mycobacte	
c 29	72.8	6.0	7542	1	CBTRXB		X75627 C.burnetii		
c 30	72.6	6.0	49617	6	AR408749		AR408749	Sequence	
c 31	72.6	6.0	49617	6	AX067453		AX067453	Sequence	
32	71.8	5.9	2556	1	AF009622		AF009622	Listeria	
c 33	71.8	5.9	324050	1	AL591983		AL591983	Listeria	

Applicant's

WD 02/18599

EP 1108770

GenBank

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 04:06:14 ; Search time 503 Seconds
(without alignments)
10227.769 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1211	100.0	1211	6	AAL42355	Aal42355 Corynebac
2	1211	100.0	309400	5	AAH68534	Aah68534 C glutami
3	603	49.8	603	5	AAH68381	Aah68381 C glutami
4	603	49.8	603	7	ACA01297	Aca01297 C. glutam
c 5	449	37.1	1185	5	AAH68383	Aah68383 C glutami
6	197	16.3	951	5	AAH68382	Aah68382 C glutami
7	197	16.3	951	7	ACA01298	Aca01298 C. glutam
8	79	6.5	1377	6	ABN89593	Abn89593 Mycobacte

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 05:05:10 ; Search time 113 Seconds
(without alignments)
5947.306 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	79.6	6.6	1443	4	US-09-221-017B-685	Sequence 685, App
	2	75	6.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	3	75	6.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	4	72.6	6.0	49617	4	US-09-596-002-28	Sequence 28, Appl
	5	69.4	5.7	1020	4	US-09-543-681A-1461	Sequence 1461, Ap
	6	63.6	5.3	933	4	US-09-134-000C-2109	Sequence 2109, Ap
	7	63.2	5.2	600	4	US-09-252-991A-14870	Sequence 14870, A
c	8	63.2	5.2	666	4	US-09-252-991A-14492	Sequence 14492, A
	9	62.6	5.2	972	4	US-09-252-991A-13278	Sequence 13278, A
c	10	62.6	5.2	1413	4	US-09-252-991A-12680	Sequence 12680, A
	11	61.8	5.1	1050	4	US-09-489-039A-4925	Sequence 4925, Ap
	12	61.2	5.1	264	4	US-09-134-001C-2660	Sequence 2660, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 06:38:32 ; Search time 531 Seconds
(without alignments)
10316.224 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggcctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*USPAP
2002 097605*

Result	Score	% Query Match	Length	DB	ID	Description
No.						
1	1211	100.0	1211	9	US-09-942-935-1	Sequence 1, Appli
2	1211	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	603	49.8	603	9	US-09-738-626-3416	Sequence 3416, Ap
c 4	449	37.1	1185	9	US-09-738-626-3418	Sequence 3418, Ap
5	197	16.3	951	9	US-09-738-626-3417	Sequence 3417, Ap
c 6	79.6	6.6	1443	13	US-10-194-163-685	Sequence 685, App
7	79	6.5	1377	15	US-10-032-201B-50	Sequence 50, Appl
8	79	6.5	4922	15	US-10-032-201B-30	Sequence 30, Appl
c 9	72.6	6.0	49617	13	US-10-672-787-28	Sequence 28, Appl
c 10	68.6	5.7	977	16	US-10-398-221-3269	Sequence 3269, Ap
c 11	63.6	5.3	5998	9	US-09-070-927A-119	Sequence 119, App
12	62.2	5.1	311	9	US-09-974-300-6285	Sequence 6285, Ap
13	60.8	5.0	1608	9	US-09-938-842A-2322	Sequence 2322, Ap
14	60.8	5.0	1608	11	US-09-938-842A-2322	Sequence 2322, Ap
15	60.4	5.0	969	15	US-10-156-761-4289	Sequence 4289, Ap
16	60.4	5.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
17	60.2	5.0	966	15	US-10-091-841-27	Sequence 27, Appl
18	60.2	5.0	966	15	US-10-032-201B-44	Sequence 44, Appl
19	58.8	4.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c 20	58.8	4.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
21	56.4	4.7	936	9	US-09-925-637-13	Sequence 13, Appl
22	56.4	4.7	936	15	US-10-084-205-13	Sequence 13, Appl
23	56.4	4.7	13086	8	US-08-781-986A-16	Sequence 16, Appl
24	56.4	4.7	13086	13	US-10-329-624-16	Sequence 16, Appl
25	55	4.5	711	15	US-10-156-761-4287	Sequence 4287, Ap
c 26	55	4.5	1286	11	US-09-764-875-63	Sequence 63, Appl
c 27	51.8	4.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
c 28	51.8	4.3	1830121	16	US-10-329-670-1	Sequence 1, Appli
29	51.2	4.2	19024	9	US-09-070-927A-179	Sequence 179, App
30	51.2	4.2	640681	9	US-09-790-988-1	Sequence 1, Appli
31	50.6	4.2	1021	15	US-10-306-292-24	Sequence 24, Appl
32	49.2	4.1	1286	13	US-10-425-114-5073	Sequence 5073, Ap
33	49.2	4.1	1325	13	US-10-425-114-3716	Sequence 3716, Ap
34	48	4.0	3249	9	US-09-738-626-3414	Sequence 3414, Ap
35	47.4	3.9	995	15	US-10-091-841-10	Sequence 10, Appl
36	47.4	3.9	995	15	US-10-091-841-23	Sequence 23, Appl
37	45.4	3.7	579	9	US-09-738-626-284	Sequence 284, App
38	45.4	3.7	1109	9	US-09-941-936A-1	Sequence 1, Appli
39	45.4	3.7	1284	13	US-10-425-114-29681	Sequence 29681, A
40	45.4	3.7	1645	13	US-10-424-599-65583	Sequence 65583, A
c 41	45.4	3.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
42	44.8	3.7	1047	16	US-10-320-797-2136	Sequence 2136, Ap
43	43.8	3.6	1403	16	US-10-320-797-1136	Sequence 1136, Ap
44	43.8	3.6	3403	16	US-10-320-797-136	Sequence 136, App
45	43	3.6	1560	15	US-10-306-292-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-942-935-1

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 05:02:41 ; Search time 2986 Seconds
(without alignments)
12110.884 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	75.2	6.2	643	14	CF418809	CF418809	USDA-FP_1
2	75.2	6.2	682	14	CF418521	CF418521	USDA-FP_1
3	75.2	6.2	690	14	CF418413	CF418413	USDA-FP_1
4	75.2	6.2	789	14	CD576244	CD576244	UCRPT01_0
5	72.4	6.0	646	12	BI096251	BI096251	S1D F05 S
6	72.2	6.0	535	9	AV628023	AV628023	AV628023
7	71.2	5.9	389	14	CF608768	CF608768	GERMO01_0
8	68.6	5.7	721	13	BQ862556	BQ862556	QGC21G18.
9	67.4	5.6	755	13	BQ863331	BQ863331	QGC23J12.
10	64.4	5.3	483	13	BQ595059	BQ595059	E012711-0
11	63	5.2	623	14	CA839585	CA839585	MCT029B08
12	63	5.2	664	14	CA840153	CA840153	MCT040C12
13	62.4	5.2	494	14	CB264406	CB264406	65-E01465
14	61	5.0	490	10	BE321389	BE321389	NF024C10I
15	61	5.0	523	10	BE321441	BE321441	NF025C10I
16	61	5.0	593	12	BG452377	BG452377	NF085C09L
17	61	5.0	609	12	BG451523	BG451523	NF110B04D
18	61	5.0	655	10	BF650364	BF650364	NF096A12E
19	61	5.0	659	10	BF636499	BF636499	NF091G04D
20	61	5.0	662	10	BE322274	BE322274	NF022E01I
21	61	5.0	663	10	AW692011	AW692011	NF046F03S
22	61	5.0	666	13	BQ139032	BQ139032	NF010C06P
23	61	5.0	667	13	BQ138990	BQ138990	NF009H09P
24	61	5.0	671	12	BG449209	BG449209	NF043G10I
25	61	5.0	683	14	CF068230	CF068230	EST668951
26	61	5.0	692	10	BF520046	BF520046	EST457514
27	61	5.0	949	14	CK291588	CK291588	EST754302
28	60.8	5.0	563	9	AW030413	AW030413	EST273668
29	60.8	5.0	564	10	BE449605	BE449605	EST356364
30	60.8	5.0	590	9	AV828748	AV828748	AV828748
31	60.2	5.0	592	12	BJ073890	BJ073890	BJ073890
32	60	5.0	504	10	BE321909	BE321909	NF045F02I
c 33	60	5.0	571	10	AW650215	AW650215	EST328669
34	59.2	4.9	345	10	BE920457	BE920457	EST424226
35	59.2	4.9	521	12	BG589427	BG589427	EST497269
36	59.2	4.9	531	10	BE920949	BE920949	EST424718
37	59.2	4.9	756	12	BG600533	BG600533	EST505428
38	59.2	4.9	869	14	CK250778	CK250778	EST734415
39	59.2	4.9	895	14	CK251220	CK251220	EST734857
40	59.2	4.9	948	14	CK258509	CK258509	EST742146
41	59.2	4.9	952	14	CK257230	CK257230	EST740867
42	59.2	4.9	982	14	CK246570	CK246570	EST730207
43	59	4.9	582	14	CA655448	CA655448	wlm0.pk00
44	57.8	4.8	615	12	BQ045955	BQ045955	EST595073
45	57.2	4.7	240	9	AV628019	AV628019	AV628019

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 07:30:51 ; Search time 4676 Seconds
(without alignments)
11225.067 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggcctttgaaaagggaat 1211

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
	1	1211	100.0	1211	6	AX394331 <i>WO 02/18579</i>	AX394331 Sequence
	2	1211	100.0	309400	6	AX127153 <i>EP</i>	AX127153 Sequence
	3	1211	100.0	325651	1	<u>AP005283</u> <i>GenBank</i>	AP005283 Corynebac
	4	603	49.8	603	6	AX123500 <i>EP</i>	AX123500 Sequence
	5	603	49.8	603	6	BD165617 <i>JP</i>	BD165617 Novel pol
c	6	449	37.1	1185	6	AX123502 <i>EP</i>	AX123502 Sequence
c	7	449	37.1	1185	6	BD165619 <i>JP</i>	BD165619 Novel pol
	8	197	16.3	951	6	AX123501 <i>EP</i>	AX123501 Sequence
	9	197	16.3	951	6	BD165618 <i>JP</i>	BD165618 Novel pol
	10	78	6.4	3457	6	AX764249 <i>WO 03/40681</i>	AX764249 Sequence
	11	78	6.4	3457	6	AX773631 <i>WO 03/46123</i>	AX773631 Sequence
<i>Pompeius</i>	12	71	5.9	3075	6	AX064225 <i>WO 01/00843</i>	AX064225 Sequence — <i>Seq: 507</i>
	13	71	5.9	3075	6	AX064311 <i>"</i>	AX064311 Sequence : <i>513</i>
	14	48	4.0	3249	6	AX123498 <i>EP</i>	AX123498 Sequence
	15	48	4.0	3249	6	BD165615 <i>JP</i>	BD165615 Novel pol
c	16	22	1.8	191712	2	BX323582	BX323582 Danio rer
c	17	21	1.7	3506	6	AX319470	AX319470 Sequence
	18	21	1.7	144699	2	AC125881	AC125881 Rattus no
c	19	21	1.7	153841	2	AC091527	AC091527 Trypanoso
	20	21	1.7	157848	10	AC091712	AC091712 Rattus no
	21	21	1.7	168843	2	AC091711	AC091711 Rattus no
c	22	21	1.7	196904	2	AC113217	AC113217 Rattus no
c	23	21	1.7	211624	10	AC114817	AC114817 Mus muscu
	24	21	1.7	242400	2	AC096829	AC096829 Rattus no
	25	21	1.7	247946	2	AC133092	AC133092 Mus muscu
	26	21	1.7	252376	2	AC105580	AC105580 Rattus no
	27	20	1.7	1302	6	AX413806	AX413806 Sequence
	28	20	1.7	2734	8	ARU421692	AJ421692 Anaptychi
c	29	20	1.7	3010	1	AF105341	AF105341 Listeria
c	30	20	1.7	37533	3	CBRG36C02	AC084560 Caenorhab
c	31	20	1.7	75650	2	AC018145	AC018145 Drosophil
	32	20	1.7	77157	8	AP004114	AP004114 Oryza sat
	33	20	1.7	87340	1	AP005224	AP005224 Corynebac

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 07:28:32 ; Search time 505 Seconds
(without alignments)
10187.263 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 3373863 seqs, 2124099041 residues
Word size : 0
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1211	100.0	1211	6	AAL42355 <i>W0-18599</i>	Aal42355 Corynebac
2	1211	100.0	309400	5	AAH68534 <i>EP</i>	Aah68534 C glutami
3	603	49.8	603	5	AAH68381 <i>EP</i>	Aah68381 C glutami
4	603	49.8	603	7	ACA01297 <i>DE 10128510</i>	Aca01297 C. glutam
c 5	449	37.1	1185	5	AAH68383 <i>EP</i>	Aah68383 C glutami
6	197	16.3	951	5	AAH68382 <i>EP</i>	Aah68382 C glutami
7	197	16.3	951	7	ACA01298 <i>DE</i>	Aca01298 C. glutam
8	78	6.4	3457	9	ADD13494 <i>W0 03/40681</i>	Add13494 C. glutam
9	71	5.9	3075	4	AAF72006 <i>W0 01/00843</i>	Aaf72006 Corynebac
10	71	5.9	3075	4	AAF72049 <i>"</i>	Aaf72049 Corynebac
11	48	4.0	3249	5	AAH68379 <i>EP</i>	Aah68379 C glutami
c 12	21	1.7	3506	6	AAI64198 <i>W0 01/83563</i>	Aai64198 <i>Rat</i> CRF2a
c 13	21	1.7	5011	9	ADD31993 <i>W0 03/110521 US</i>	Add31993 Rat corti
14	20	1.7	28	6	AAL42358	Aal42358 Corynebac
c 15	20	1.7	28	6	AAL42359	Aal42359 Corynebac

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 08:35:47 ; Search time 114 Seconds
(without alignments)
5895.136 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match Length DB	ID	Description				
c 1	19	1.6 963 4	US-09-252-991A-2989	Sequence 2989, Ap				
2	19	1.6 1431 4	US-09-252-991A-2787	Sequence 2787, Ap				
c 3	19	1.6 1707 4	US-09-252-991A-3180	Sequence 3180, Ap				
c 4	19	1.6 1709 4	US-08-936-165A-188	Sequence 188, App				
5	18	1.5 2069 1	US-07-921-178A-1	Sequence 1, Appli				
c 6	18	1.5 1230025 4	US-09-198-452A-1	Sequence 1, Appli				
c 7	17	1.4 404 2	US-08-951-648-33	Sequence 33, Appl				
c 8	17	1.4 404 3	US-09-174-437-33	Sequence 33, Appl				
c 9	17	1.4 404 4	US-09-686-055A-33	Sequence 33, Appl				
10	17	1.4 453 4	US-09-543-681A-3969	Sequence 3969, Ap				
11	17	1.4 495 4	US-09-252-991A-15616	Sequence 15616, A				
c 12	17	1.4 528 2	US-08-687-080-83	Sequence 83, Appl				

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 10:11:48 ; Search time 532 Seconds
(without alignments)
10296.833 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2936184 seqs, 2261732022 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Nakagawa

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1211	100.0	1211	9	US-09-942-935-1		Sequence 1, Appli
2	1211	100.0	3309400	9	US-09-738-626-1		Sequence 1, Appli
3	603	49.8	603	9	US-09-738-626-3416		Sequence 3416, Ap
c 4	449	37.1	1185	9	US-09-738-626-3418		Sequence 3418, Ap
5	197	16.3	951	9	US-09-738-626-3417		Sequence 3417, Ap
6	48	4.0	3249	9	US-09-738-626-3414		Sequence 3414, Ap
c 7	21	1.7	3506	9	US-09-847-852-1		Sequence 1, Appli
c 8	21	1.7	5011	15	US-10-293-702-1		Sequence 1, Appli
9	20	1.7	1302	16	US-10-398-221-797		Sequence 797, App
c 10	19	1.6	300	15	US-10-156-761-1964		Sequence 1964, Ap
c 11	19	1.6	1709	9	US-09-939-980-188		Sequence 188, App
12	19	1.6	3062	13	US-10-282-122A-31528		Sequence 31528, A
13	19	1.6	6378	15	US-10-311-455-149		Sequence 149, App
14	19	1.6	9025608	15	US-10-156-761-1		Sequence 1, Appli
c 15	18	1.5	434	13	US-10-027-632-86208		Sequence 86208, A
c 16	18	1.5	434	13	US-10-027-632-178940		Sequence 178940,
c 17	18	1.5	434	16	US-10-027-632-86208		Sequence 86208, A
c 18	18	1.5	434	16	US-10-027-632-178940		Sequence 178940,
c 19	18	1.5	567	15	US-10-156-761-5054		Sequence 5054, Ap
c 20	18	1.5	648	13	US-10-027-632-8947		Sequence 8947, Ap
c 21	18	1.5	648	16	US-10-027-632-8947		Sequence 8947, Ap
c 22	18	1.5	678	13	US-10-027-632-273855		Sequence 273855,
c 23	18	1.5	678	16	US-10-027-632-273855		Sequence 273855,
24	18	1.5	749	13	US-10-027-632-11318		Sequence 11318, A
25	18	1.5	749	13	US-10-027-632-11319		Sequence 11319, A
26	18	1.5	749	16	US-10-027-632-11318		Sequence 11318, A
27	18	1.5	749	16	US-10-027-632-11319		Sequence 11319, A
28	18	1.5	1590	16	US-10-369-493-37601		Sequence 37601, A
29	18	1.5	1914	16	US-10-369-493-28918		Sequence 28918, A
c 30	18	1.5	2000	9	US-09-887-576-852		Sequence 852, App
31	18	1.5	2069	12	US-10-152-319A-1639		Sequence 1639, Ap
32	18	1.5	4383	16	US-10-369-493-46057		Sequence 46057, A
c 33	18	1.5	6170	13	US-10-363-616-184		Sequence 184, App
c 34	18	1.5	10907	16	US-10-429-802-31		Sequence 31, Appl
c 35	18	1.5	10907	16	US-10-430-503-22		Sequence 22, Appl
c 36	18	1.5	11460	13	US-10-415-058-7		Sequence 7, Appli
37	18	1.5	69300	13	US-10-415-058-6		Sequence 6, Appli
c 38	18	1.5	91552	13	US-10-415-058-5		Sequence 5, Appli
c 39	18	1.5	119596	15	US-10-270-336-3		Sequence 3, Appli
40	18	1.5	185555	13	US-10-087-192-1999		Sequence 1999, Ap
41	18	1.5	653122	13	US-10-087-192-226		Sequence 226, App
c 42	18	1.5	1230025	16	US-10-289-762-1		Sequence 1, Appli
c 43	17	1.4	116	9	US-09-966-880A-14		Sequence 14, Appl
c 44	17	1.4	120	9	US-09-969-373-1351		Sequence 1351, Ap
45	17	1.4	173	9	US-09-864-761-26899		Sequence 26899, A

ALIGNMENTS

RESULT 1
US-09-942-935-1

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 08:33:17 ; Search time 2985 Seconds
(without alignments)
12114.942 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca.....ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	22	1.8	618	12	BG656707	BG656707 df47b06.y
c	2	22	1.8	852	14	CD252970	CD252970 AGENCOURT
c	3	21	1.7	358	29	TA58F03Q	AL455737 T. brucei
	4	21	1.7	558	28	AZ387580	AZ387580 1M0147G09
c	5	20	1.7	479	28	AZ552929	AZ552929 RPCI-23-1
c	6	20	1.7	636	28	AZ241095	AZ241095 RPCI-23-3
	7	20	1.7	794	9	AI439244	AI439244 ti59a03.x
	8	20	1.7	971	12	BG393115	BG393115 602411384
	9	19	1.6	285	28	CC112112	CC112112 NDL.23C11
	10	19	1.6	290	28	CC142352	CC142352 NDL.69F6.
c	11	19	1.6	300	9	AU231710	AU231710 AU231710
	12	19	1.6	308	28	CC013856	CC013856 PUEBF69TD
	13	19	1.6	317	10	BE364026	BE364026 PI1_11_F0
c	14	19	1.6	380	14	CD814439	CD814439 BN15.023B
	15	19	1.6	380	28	BH877108	BH877108 hr35e11.b
	16	19	1.6	387	28	BZ331847	BZ331847 hx23d03.g
	17	19	1.6	411	28	BZ648869	BZ648869 OGAOP23TC
	18	19	1.6	419	12	BP099919	BP099919 BP099919
c	19	19	1.6	428	28	BZ346375	BZ346375 hv18b09.b
	20	19	1.6	442	14	CD003371	CD003371 EST1504 N
c	21	19	1.6	445	28	BH127538	BH127538 G-1h21.f
	22	19	1.6	452	28	BH710348	BH710348 BOMBV59TF
	23	19	1.6	460	28	AZ696294	AZ696294 RPCI-23-2
	24	19	1.6	465	28	BH869577	BH869577 hl45f07.g
	25	19	1.6	478	12	BI419494	BI419494 LjNEST40f
	26	19	1.6	478	14	CF053940	CF053940 QCN22g05.
c	27	19	1.6	486	28	AQ934851	AQ934851 RPCI-23-2
	28	19	1.6	490	28	CC156727	CC156727 ig15b10.b
	29	19	1.6	502	13	BQ533490	BQ533490 LEAF4_22_
	30	19	1.6	503	28	BZ315255	BZ315255 ia56f04.b
	31	19	1.6	524	28	BZ333551	BZ333551 hx70h12.g
c	32	19	1.6	527	13	BQ588119	BQ588119 E012337-0
	33	19	1.6	539	28	CC166564	CC166564 ii54h04.b
	34	19	1.6	547	28	BZ309344	BZ309344 ic06a10.b
	35	19	1.6	556	29	PT022K05R	AL446773 Parameciu
c	36	19	1.6	559	29	CNS02DIZ	AL192500 Tetraodon
	37	19	1.6	560	28	BZ336835	BZ336835 hz39e06.b
	38	19	1.6	561	28	BZ628389	BZ628389 ih59h05.g
	39	19	1.6	578	28	BZ305613	BZ305613 hw56b06.b
	40	19	1.6	584	13	CA035588	CA035588 4001314 B
c	41	19	1.6	585	28	BZ165599	BZ165599 CH230-277
c	42	19	1.6	588	28	BZ648875	BZ648875 OGAOP23TM
c	43	19	1.6	589	28	BZ331908	BZ331908 hx23h11.g
c	44	19	1.6	590	28	AQ753987	AQ753987 HS_5395_B
c	45	19	1.6	591	29	PT017E15U	AL447151 Parameciu

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 11:03:58 ; Search time 2848 Seconds
(without alignments)
3409.003 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDGTGCVQPA.....ALLHADFFGPDGSIQCESN 224

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-

Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083425_11920/app_query.fasta_1
.391

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_CGN_1_1_4958@runat_30042004_083425_11920 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result	Query							
No.	Score	Match	Length	DB	ID		Description	
<hr/>								
1	1159	100.0	1211	6	AX394331	AX394331	Sequence	
2	1159	100.0	309400	6	AX127153	AX127153	Sequence	
3	1159	100.0	325651	1	AP005283	AP005283	Corynebac	
4	1037	89.5	603	6	AX123500	AX123500	Sequence	
5	1037	89.5	603	6	BD165617	BD165617	Novel pol	
6	652	56.3	87340	1	AP005224	AP005224	Corynebac	
7	348.5	30.1	53793	1	BX248361	BX248361	Corynebac	
8	282.5	24.4	278492	1	BX248347	BX248347	Mycobacte	
9	280.5	24.2	14563	1	AE007193	AE007193	Mycobacte	
10	272.5	23.5	244800	1	BX842584	BX842584	Mycobacte	
c 11	264.5	22.8	35336	1	MSGY367	AD000008	Mycobacte	
c 12	253	21.8	303550	1	SCO939118	AL939118	Streptomy	
13	249.5	21.5	300425	1	AP005038	AP005038	Streptomy	
14	245	21.1	4026	1	SCO007313	AJ007313	Streptomy	
c 15	242	20.9	1185	6	AX123502	AX123502	Sequence	
c 16	242	20.9	1185	6	BD165619	BD165619	Novel pol	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 11:02:03 ; Search time 345 Seconds
(without alignments)
2758.250 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTCVPPQA.....ALLHADFFGPEDGSIQCESN 224

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-

Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083424_11908/app_query.fasta_1.391

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_@CGN_1_1_885_@runat_30042004_083424_11908 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	1159	100.0 1211	6	AAL42355	Aal42355 Corynebac
	2	1159	100.0 309400	5	AAH68534	Aah68534 C glutami
	3	1037	89.5 603	5	AAH68381	Aah68381 C glutami
	4	1037	89.5 603	7	ACA01297	Aca01297 C. glutam
	5	280.5	24.2 103765	4	AAI99683_43	Continuation (44 o
	6	272.5	23.5 11529	4	AAI99682_44	Continuation (45 o
	7	272.5	23.5 110000	4	AAI99682_43	Continuation (44 o
c	8	242	20.9 1185	5	AAH68383	Aah68383 C glutami
	9	221.5	19.1 639	5	AAH66206	Aah66206 C glutami
	10	221.5	19.1 648	7	ACA00415	Aca00415 C. glutam
	11	221.5	19.1 1330	6	AAD35114	Aad35114 Corynebac
	12	221.5	19.1 2086	6	AAD35115	Aad35115 Corynebac
	13	221.5	19.1 349980	5	AAH68527	Aah68527 C glutami
	14	211.5	18.2 647	2	AAQ70249	Aaq70249 P. aerugi
	15	211.5	18.2 647	2	AAQ70242	Aaq70242 P. aerugi
	16	211.5	18.2 647	3	AAA51919	Aaa51919 P. aerugi
	17	205	17.7 570	7	ACF71991	Acf71991 Photorhab
	18	205	17.7 110000	7	ACF67367_51	Continuation (52 o
	19	205	17.7 110000	7	ACF67367_52	Continuation (53 o
	20	205	17.7 110000	7	ACF65387_3	Continuation (4 of
	21	201	17.3 110000	2	AAT42063_06	Continuation (7 of
	22	194	16.7 771	6	ABT05614	Abt05614 Mycobacte
	23	194	16.7 771	7	ABZ71111	Abz71111 Mycobacte
	24	194	16.7 75216	6	ABX09141	Abx09141 Mycobacte
	25	194	16.7 110000	4	AAI99682_13	Continuation (14 o
	26	194	16.7 110000	4	AAI99683_13	Continuation (14 o
	27	193.5	16.7 38675	9	ADB74386	Adb74386 Mycobacte
c	28	178	15.4 14615	4	AAS59577	Aas59577 Propionib
c	29	178	15.4 14615	7	ACF64506	Acf64506 Propionib
	30	169.5	14.6 579	5	AAH65249	Aah65249 C glutami
	31	169.5	14.6 579	7	ACA01964	Aca01964 C. glutam
	32	169.5	14.6 1109	6	AAD33874	Aad33874 Corynebac
c	33	169.5	14.6 349980	5	AAH64966	Aah64966 C glutami
	34	164.5	14.2 564	6	ABK74063	Abk74063 Bacillus
	35	160.5	13.8 603	3	AAA64868	Aaa64868 Bordetell
c	36	160.5	13.8 35026	3	AAA64890	Aaa64890 Bordetell
c	37	153.5	13.2 747	7	ACF65615	Acf65615 Photorhab
	38	153	13.2 651	3	AAA39563	Aaa39563 M. tuberc
c	39	153	13.2 110000	4	AAI99682_35	Continuation (36 o
c	40	153	13.2 110000	4	AAI99683_35	Continuation (36 o
	41	146.5	12.6 37856	3	AAA11992	Aaa11992 S. cellul
	42	144	12.4 110000	4	AAI99682_23	Continuation (24 o
	43	144	12.4 110000	4	AAI99683_23	Continuation (24 o
c	44	142.5	12.3 735	7	ACF65674	Acf65674 Photorhab
c	45	140	12.1 110000	4	AAI99682_37	Continuation (38 o

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 12:09:03 ; Search time 85 Seconds
(without alignments)
1462.459 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTCVPQPA.....ALLHADFFGPEDGSIQCEN 224

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

-Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083426_11947/app_query.fasta_1.391

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_CGN_1_1_103_@runat_30042004_083426_11947 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	280.5	24.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
2	272.5	23.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
3	211.5	18.2	647	1	US-08-260-202A-9	Sequence 9, Appli
4	211.5	18.2	647	1	US-08-017-114-9	Sequence 9, Appli
5	211.5	18.2	647	3	US-08-505-307-9	Sequence 9, Appli
6	211.5	18.2	647	4	US-09-609-151A-9	Sequence 9, Appli
7	211.5	18.2	647	5	PCT-US94-02034-9	Sequence 9, Appli
8	211.5	18.2	840	4	US-09-252-991A-13069	Sequence 13069, A
9	201	17.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
10	201	17.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
11	193.5	16.7	615	4	US-09-489-039A-4559	Sequence 4559, Ap
12	193.5	16.7	38675	4	US-08-311-731A-135	Sequence 135, App
13	188	16.2	600	4	US-09-543-681A-3510	Sequence 3510, Ap
c 14	153	13.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 15	153	13.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
16	141.5	12.2	846	4	US-09-252-991A-9635	Sequence 9635, Ap
c 17	141.5	12.2	1062	4	US-09-252-991A-9532	Sequence 9532, Ap
18	141.5	12.2	1371	4	US-09-252-991A-9717	Sequence 9717, Ap
c 19	132	11.4	6464	4	US-09-221-017B-168	Sequence 168, App
20	128	11.0	540	4	US-09-134-000C-1484	Sequence 1484, Ap
21	127	11.0	603	4	US-09-134-000C-797	Sequence 797, App
c 22	124	10.7	9837	4	US-09-221-017B-636	Sequence 636, App
23	112	9.7	597	4	US-09-252-991A-13522	Sequence 13522, A
24	106.5	9.2	525	4	US-09-107-532A-1956	Sequence 1956, Ap
25	106.5	9.2	621	4	US-09-252-991A-1369	Sequence 1369, Ap
c 26	105	9.1	1239	4	US-09-252-991A-12715	Sequence 12715, A
c 27	103.5	8.9	1753	4	US-09-221-017B-1063	Sequence 1063, Ap
c 28	102	8.8	1524	4	US-09-252-991A-1651	Sequence 1651, Ap
29	102	8.8	1770	4	US-09-252-991A-1522	Sequence 1522, Ap
30	99.5	8.6	717	4	US-09-328-352-2206	Sequence 2206, Ap
c 31	99	8.5	129908	4	US-09-585-858-1	Sequence 1, Appli
c 32	98.5	8.5	894	4	US-09-252-991A-1599	Sequence 1599, Ap
33	89	7.7	819	4	US-09-252-991A-11741	Sequence 11741, A
c 34	89	7.7	1686	4	US-09-252-991A-11503	Sequence 11503, A
35	89	7.7	1920	4	US-09-252-991A-11882	Sequence 11882, A
c 36	88	7.6	1872	4	US-09-252-991A-6335	Sequence 6335, Ap
37	88	7.6	2112	4	US-09-252-991A-6212	Sequence 6212, Ap
38	87.5	7.5	1553	4	US-09-620-312D-490	Sequence 490, App
39	86	7.4	1548	2	US-08-762-106-5	Sequence 5, Appli
40	86	7.4	1548	3	US-09-320-774-5	Sequence 5, Appli
41	85.5	7.4	1497	4	US-09-489-039A-6536	Sequence 6536, Ap
42	84.5	7.3	2220	4	US-09-540-236-863	Sequence 863, App
c 43	84.5	7.3	94750	4	US-09-596-002-38	Sequence 38, Appl
44	84	7.2	1758	4	US-09-252-991A-490	Sequence 490, App
c 45	84	7.2	1794	4	US-09-252-991A-568	Sequence 568, App

ALIGNMENTS

RESULT 1
US-09-103-840A-2
; Sequence 2, Application US/09103840A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 13:19:54 ; Search time 357 Seconds
(without alignments)
2838.252 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTCVPQPA.....ALLHADFFGPEGDSIQCESN 224

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083427_12038/app_query.fasta_1.391

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09942935_@CGN_1_1_107_@runat_30042004_083427_12038
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

```

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1159	100.0	1211	9	US-09-942-935-1	Sequence 1, Appli
2	1159	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	1037	89.5	603	9	US-09-738-626-3416	Sequence 3416, Ap
4	249.5	21.5	711	15	US-10-156-761-4287	Sequence 4287, Ap
5	249.5	21.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 6	242	20.9	1185	9	US-09-738-626-3418	Sequence 3418, Ap
7	221.5	19.1	639	9	US-09-738-626-1241	Sequence 1241, Ap
8	221.5	19.1	1330	9	US-09-935-757-1	Sequence 1, Appli
9	221.5	19.1	2086	9	US-09-935-757-5	Sequence 5, Appli
c 10	201.5	17.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
11	201	17.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
12	201	17.3	1830121	16	US-10-329-670-1	Sequence 1, Appli
13	198	17.1	657	15	US-10-156-761-3104	Sequence 3104, Ap
14	194	16.7	75216	15	US-10-080-170-646	Sequence 646, App
15	182.5	15.7	681	15	US-10-156-761-3025	Sequence 3025, Ap
16	169.5	14.6	579	9	US-09-738-626-284	Sequence 284, App
17	169.5	14.6	1109	9	US-09-941-936A-1	Sequence 1, Appli
c 18	169.5	14.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
19	164.5	14.2	564	9	US-09-974-300-1354	Sequence 1354, Ap
20	150.5	13.0	594	15	US-10-156-761-5107	Sequence 5107, Ap
21	149	12.9	612	15	US-10-156-761-886	Sequence 886, App
22	147.5	12.7	618	15	US-10-156-761-6054	Sequence 6054, Ap
23	145	12.5	651	15	US-10-156-761-606	Sequence 606, App
24	137.5	11.9	618	9	US-09-738-626-855	Sequence 855, App
25	137.5	11.9	1148	9	US-09-942-936-1	Sequence 1, Appli
26	135	11.6	546	13	US-10-282-122A-12529	Sequence 12529, A
27	134	11.6	576	15	US-10-156-761-3305	Sequence 3305, Ap
28	132.5	11.4	537	15	US-10-156-761-4690	Sequence 4690, Ap
c 29	132	11.4	6464	13	US-10-194-163-168	Sequence 168, App
30	130.5	11.3	577	9	US-09-974-300-1365	Sequence 1365, Ap
31	130	11.2	1002	15	US-10-156-761-3350	Sequence 3350, Ap
32	129.5	11.2	526	9	US-09-974-300-1380	Sequence 1380, Ap
33	129.5	11.2	537	15	US-10-156-761-4048	Sequence 4048, Ap
34	129.5	11.2	540	9	US-09-974-300-5795	Sequence 5795, Ap
35	129.5	11.2	546	15	US-10-156-761-7271	Sequence 7271, Ap
36	128	11.0	24601	9	US-09-070-927A-223	Sequence 223, App
c 37	127	11.0	10636	9	US-09-070-927A-74	Sequence 74, Appl
38	125.5	10.8	612	15	US-10-156-761-1204	Sequence 1204, Ap
39	125	10.8	618	15	US-10-156-761-3338	Sequence 3338, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 12:06:28 ; Search time 2506 Seconds
(without alignments)
2669.245 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDGTGCVQPA.....ALLHADFFGPEDGSIQCESN 224

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083425_11934/app_query.fasta_1.391

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935@cgn_1_1_3549@runat_30042004_083425_11934 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	174	15.0	879	11	BC022210		BC022210	Homo sapi
c	2	154.5	13.3	761	28	BH242195		BH242195	ATZFD48TF
	3	148	12.8	893	13	BQ931778		BQ931778	AGENCOURT
	4	146.5	12.6	968	28	BZ561490		BZ561490	pacs2-164
	5	139	12.0	321	13	BU275590		BU275590	Cr_Emb_04
c	6	130	11.2	943	28	BZ552424		BZ552424	pacs1-60_
	7	117.5	10.1	542	28	BH823104		BH823104	BACPP18-H
	8	117.5	10.1	626	28	BH832826		BH832826	BACPP4-G1
c	9	116	10.0	573	28	BH391760		BH391760	AG-ND-148
c	10	111	9.6	436	28	BH403298		BH403298	AG-ND-132
c	11	111	9.6	742	28	BH393492		BH393492	AG-ND-138
	12	109.5	9.4	804	28	BH242457		BH242457	ATZFC44TF
c	13	109.5	9.4	1844	28	BH614306		BH614306	1C22/2B8_
c	14	109.5	9.4	1844	28	BH614501		BH614501	2B8_Conti
c	15	109	9.4	456	28	BH374042		BH374042	AG-ND-143
c	16	105.5	9.1	375	28	AZ576920		AZ576920	03a11 Sho
	17	105	9.1	1052	13	BU857304		BU857304	AGENCOURT
	18	104	9.0	872	28	BH372133		BH372133	AG-ND-133
	19	102.5	8.8	768	14	CK029060		CK029060	AGENCOURT
	20	102.5	8.8	793	14	CF347223		CF347223	AGENCOURT
	21	102.5	8.8	1083	14	CB923509		CB923509	STR00853
c	22	102	8.8	1012	28	BZ573065		BZ573065	msh2_2928
c	23	101.5	8.8	698	14	CB851398		CB851398	UI-CF-DU1
c	24	101.5	8.8	797	14	CF891232		CF891232	UI-CF-DU1
c	25	101	8.7	768	28	BZ675390		BZ675390	PUBKV84TD
	26	101	8.7	795	12	BI704389		BI704389	zfshTARAM
	27	100.5	8.7	2321	11	AY108097		AY108097	Zea mays
	28	97.5	8.4	713	13	BQ616834		BQ616834	faa95g01.
	29	97	8.4	683	13	BX847466		BX847466	BX847466